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FIG. 1

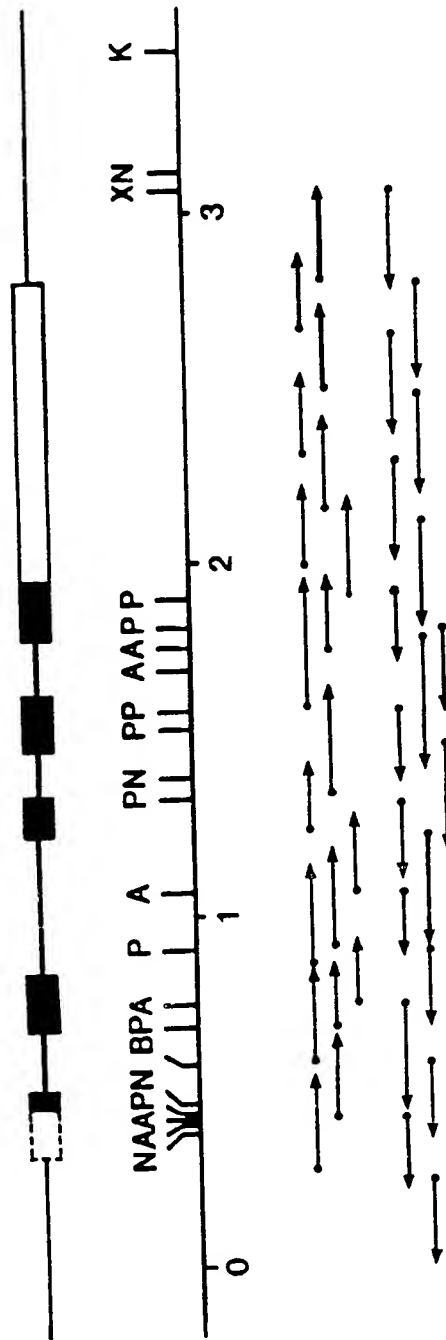


FIG. 2A

[illegible]

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FIG. 2B

110 Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly
 CTG CAG CTG GAC GTC GAC GAC TTT GCC ACC ACC ATC TGG CAG CAG ATG GAA GAA CTG GGA
 GAC GTC GAC CTG CAG CAG CGG CTG AAA CGG TGG TGG TAG ACC GTC GTC TAC CTT CTT GAC CCT

120

130 Met Ala Pro Ala Gln Leu Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
 ATG GCC CCT GCC CTG CAG CCC ACC ACC CAG GGT GCC ATG CCG GCC TTC GCC TCT GCT TTC CAG
 TAC CGG GGA CGG GAC GTC GAC GTC GGG TGG CTC CCA CGG TAC GGC CGG AAG CGG AGA CGA AAG GTC

140

150 Arg Arg Ala Gly Gln Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr
 CGC CGG GCA GGA GGG GTC CTG GTC GGT GTC TCC CAT CTG CAG AGC TTC CTG GAG GTG TCG TAC
 GCG GCC CGT CCT CCC CAG GAC CAA CGG AGG GTA GAC GTC TCG AAG GAC CTC CAC AGC ATG

160

170 Arg Val Leu Arg His Leu Ala Gln Pro OP
 CGC GTT CTA CGC CAC CTT GCC CAG CCC TGA GCC AAG CCC TCC CCA TCC CAT GTA TTT ATC
 CGC CAA GAT GCG GTG GAA CGG GTC GGG ACT

174

TCT ATT TAA TAT TTA TGT CTA TTT AAG CCT CAT ATT TAA AGA CAG GGA AGA GCA GAA CGG

AGC CCC AGG CCT CTG TGT CCT TCC CTG CAT TTC TGA GTT TCA TTC TCC TGC CTG TAG CAG

Stul

TGA GAA AAA GCT CCT GTC CTC CCA TCC CCT GGA CTG GGA GGT AGA TAG GTA AAT ACC AAG

TAT TTA TTA CTA TGA CTG CTC CCC AGC CCT GGC TCT GCA ATG GGC ACT GGG ATG AGC CGC

TGT GAG CCC CTG GTC CTG AGG GTC CCC ACC TGG GAC CCT TGA GAG TAT CAG GTC TCC CAC

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FIG. 2C

GTC GGA GAC AAG AAA TCC CTG TTT AAT ATT TAA ACA GCA GTG TTC CCC ATC TGG GTC CTT
GCA CCC CTC ACT CTG GCC TCA GCC GAC TGC ACA GCG GCC CCT GCA TCC CCT TGG CTG TGA
GGC CCC TGG ACA AGC AGA GGT GGC CAG AGC TGG GAG GCA TGG CCC TGG GGT CCC ACG AAT
TTG CTG GGG AAT CTC GTT TTT CTT AAG ACT TTT GGG ACA TGG TTT GAC TCC CGA ACA
TCA CCG ACG TGT CTC CTG TTT TTC TGG GTG GCC TCG GGA CAC CTG CCC TGC CCC CAC GAG
GGT CAG GAC TGT GAC TCT TTT TAG GGC CAG GCA GGT GCC TGG ACA TTT GCC TTG CTG GAC
GGG GAC TGG GGA TGT GGG AGG GAG CAG ACA GGA GGA ATC ATG TCA GGC CTG TGT GTG AAA
GGA AGC TCC ACT GTC ACC CTC CAC CTC TTC ACC CCC CAC TCA CCA GTG TCC CCT CCA CTG
TCA CAT TGT AAC TGA ACT TCA GGA TAA AGT GTT TGC CTC CA

StuI

[f150-200 base poly A plus 25-30 bases plasmid DNA preceding a PvuII restriction site]-3'

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GGGGACAGGCTTGAGAAATCCCAAAGGAGAGGGGCAAGGACACTGCCCCCGCAAGTCTGCCAGAGCAGAG 70
AGGGAGACCCGACTCAGCTGCCACTTCCCCACAGGCTCGTGCCGCTTCCAGGCGTCTATCAGCGGCTCA 140
GCCTTGTTCAGCTGTTCTGTCAAACA CTCTGGGGCCATT CAGGCCCTGGGTGGGCAGCGGGAGGAAGG 210
GAGTTGAGGGGGGCAAGCGACGTCAAAGGAGGATCAGAGATTCACAAATTTACAAAACTTTCGCAAA 280
CAGCTTTTGTTCCAAACCCCTTGCAATTGCTTGGACACCAAAATTTGCATAAAATCCTGGGAAGTTATTAC 350
TAAGCCTTAGTCGTGGCCCCCAGGTAATTTCTCCAGGCCCTCCATGGGGTTATGTATAAAGGCCCCCTTA 420
GAGCTGGGCCCCAAAACAGCCCCGGAGCCTGCAGCCCCAGCCCCACCCAGACCCCATGGCTGGACCTGCCACC 490
GlnSerProMetLysLeuMeta
CAGAGCCCATGAAGCTGATGGGTGAGTGTCTTGGCCCCAGGATGGGAGAGCCGCTGCCCTGGCATGGGA 560
GGGAGGCTGGTGTACAGAGGGGCTGGGGATCCCCGTTCTGGGAATGGGGATTAAAGGCACCCAGTGTCC 630
CCGAGAGGGCCTCAGGTGGTAGGGAACAGCATGTCTCCTGAGCCCCGCTCTGTCCCCAGCCCTGCAGCTGC 700
1aLeuGlnLeuL

FIG. 3A

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-10	-1	+	10
euLeuTrpHisSerAlaLeuTrpThrValGlnGluAlaThrProLeuGlyProAlaSerSerLeuProGlu			770
TGCTGTGGCACAGTGCACTCTGGACAGTGCAGGAAGCCACCCCTGGGCCCTGCCAGCTCCTGTGCCCA			
	20	30	
nSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLys			840
GAGCTTCCTGCTCAAGTGCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAAG			
35			910
Leu			
CTGTGTAGTGAGGTGGGTGAGAGGGCTGTGGAGGGAAGCCCGTGGGGAGAGCTAAGGGGGATGGAACTG			
			980
CAGGGCCAACATCCTCTGGAAGGACATGGGAGAATATTAGGAGCATGGAGCTGGGGAAGGCTGGGAAG			
			1050
GGACTTGGGGAGGAGGACCTTGGTGGGGACAGTGCTCGGGAGGGCTGGCTGGGATGGGAGTGGAGGCATC			
			1120
ACATTCAGGAGAAAGGGCAAGGGCCCTGTGTGAGATCAGAGAGTGGGGTGCGAGGCAGAGAGGAACTGAA			
			1190
CAGCCTGGCAGGACATGGAGGGAGGGGAAAGACCAGAGAGTCGGGGAGGACCCGGGAAGGAGCGGCGACC			
	36	40	
	CysAlaThrTyrLysLeuCysHisProGlu		
			1260
CGGCCACGGCGAGTCTCACTCAGCATCCTTCCATCCCCAGTGTGCCACCTACAAGCTGTGCCACCCCGAG			
	60		
GluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaIle			1330
GAGCTGGTGCTCGGACACTCTCTGGGCATCCCCCTGGGCTCCCCAGTGTGCCACCCAGCGCCC			

FIG. 3B

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70 71
 euGlnLeu 1400
 TGCAGCTGGTGAGTGT CAGGAAAGGATAAGGCTAATGAGGAGGGGGAAGGAGAGGAAACACCCATGGG
 1470
 CTCCCCCATGTCTCCAGGTTCCAAGCTGGGGGCTGACGTATCTCAGGCAGCACCCCTAACTCTTCCGC
 90
 72 AlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnA
 1540
 TCTGTCTCACAGGCAGGCTGCTTGAGCCAACTCCATAGCGGCCCTTTCTCTACCAAGGGCTCCTGCAGG
 110
 100 laLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAl
 1610
 CCCTGGAAAGGATCTCCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTGCCGACTTTGC
 120
 aThrThrIleTrpGlnGln 1680
 CACCACCATCTGGCAGCAGGTGAGCCCTTGTGGCAGGGTGGCCCAAGTCTGTGGCATTTCTGGGCACC
 1750
 ACAGCCGGCCCTGTGTATGGGCCCTGTCCATGCTGTCAAGCCCCCAGCATTTCCCTCATTTGTAATAACGCC
 121
 MetGluGluLeuGlyMetAlaProAla
 1820
 CACTCAGAAGGGCCCAACCACTGATCACAGCTTTCCCCCACCAGATGGAAGAACTGGGAATGGCCCCCTGCC
 150
 130 LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgAlaGlyGlyValLeuV
 1890
 CTGCAGCCCCACCCAGGGTGCCATGCCGGCCTTCGCCCTCTGCTTCCAGCGCCGGCAGGAGGGTCCCTGG

FIG. 3C

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160 170 174
alAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnProOP 1960
TTGCCCTCCCATCTGCAGAGCTTCCTGGAGGTGTCGTACCGCTTCTACGCCACCTTGCCCCAGCCCTGAGC
2030
CAAGCCCTCCCCATCCCATGTATTTATCTCTATTTAATAATTTATGTCTATTTAAGCCTCATATTTAAAGA
2100
CAGGGAAGAGCAGAACGGAGCCCCAGGCCCTCTGTGTCTTCCCCTGCATTTCTGAGTTTCATTTCTCTCCCTGCC
2170
TGTAAGCAGTGAGAAAAAGCTCCTGTCTCTCCATCCCTGGACTGGGAGGTAGATAGGTAAATACCAAGTA
2240
TTTATTACTATGACTGCTCCCCAGCCCCCTGGCTCTGCAATGGGCACCTGGGATGAGCCGCTGTGAGCCCCCTG
2310
GTCCTGAGGGTCCCCACCTGGGACCCCTTGAGAGTATCAGGTCTCCACACGTGGGAGACAAGAAATCCCTGT
2380
TTAATAATTAAACAGCAGTGTTCCTCCCATCTGGGTCTTGCACTTGGCCTCAGCCGACTGCAC
2450
AGCGGCCCTGCATCCCCCTTGGCTGTAGGCCCTGGACAAGCAGAGGTGGCCAGAGCTGGGAGGCATGG
2520
CCCTGGGGTCCCACGAATTGCTGGGGAATCTCGTTTCTTCTTAAAGACTTTTGGGACATGGTTTGACT
2590
CCCGAACATCACCGACGTCTCCTGTTTTTCTGGGTGGCCTCGGGACACCTGCGCCTGCCCCCACGAGGG

FIG. 3D

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TCAGGACTGTACTCTTTTAGGGCCAGGCAGGTGCCCTGGACATTTGCCCTTGCTGGATGGGGACTGGGGA 2660

TGTGGGAGGGAGCAGACAGGAGGAATCATGTCAGGCCCTGTGTGTGAAAGGAAGCTCCACTGTCAACCCTCC 2730

ACCTCTTCACCCCCACTCAACAGTGTCCCCCTCCACTGTCAATGTAACTGAACCTTCAGGATAATAAAG 2800

TGTTTGCCCTCCAGTCACGTCCTTCCCTCCTTCTTGAGTCCAGCTGGTGCCCTGGCCAGGGGCTGGGGAGGTG 2870

GCTGAAGGGTGGGAGAGGCCAGAGGGAGGTCGGGGAGGAGGTCCTGGGGAGGAGGTCAGGGAGGAGGAGG 2940

AAAGTTCTCAAGTTCGTCTGACATTCAATCCGTTAGCACATATTTATCTGAGCACCTACTCTGTGCAGAC 3010

GCTGGGCTAAGTGCTGGGGACACAGCAGGGGAACAAGGCAGACATGGAATCTGCACTCGAG 3070

FIG. 3E

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FIG. 4

EChpG-CSFDNA SECTION I

10 1 20 30 40 50 60
 CTAGAAAA ACCAAGGAGG TAATAAATAA TGACTCCATT AGGTCCTGGT TCTTCTCTGC
 TTTT TGGTTCCTCC ATTATTTATT ACTGAGGTAA TCCAGGACGA AGAAGAGACG

8XbaI

70 3 80 90 100 110 120
 CGCAAGCCTT TCTGCTGAAA TGTCCTGGAAC AGGTTTCGTAA AATCCAGGGT GACGGTGCTG
 GCGTTTCGAA AGACGACTTT ACAGACCTTG TCCAAGCATT TTAGGTCCCA CTGCCACGAC

1011

130 5 140 150 160 170 180
 CACTGCAAGA AAAACTGTGC GCTACTTACA AACTGTGCCA TCCGGAAGAG CTGGTACTGC
 GTGACGTTCT TTTTGACACG CGATGAATGT TTGACACGGT AGGCTTCTG GACCATGACG

1213

7 190 100
 TGGGTCATTC TCTTGG
 ACCCAGTAAG AGAACCCCTAG

14BamHI

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FIG. 5

EChpG-CSFDNA SECTION II

10 15 20 30 40 50 60
 GATCCCGTG GGCTCCGGCTG TCTTCTTGTC CATCTCAAGC TCTTCAGCTG GCTGGTTGTC
 GGCAC CCGAGGCGAC AGAAGAACAG GTAGAGTTCTG AGAAGTCGAC CGACCAACAG
 23 24

BamHI

70 17 80 90 110 120
 TGCTCTCAACT GCATTCTGGT CTGTTCCCTGT ATCAGGGTCT TCTGCAAGCT CTGGAAGGTA
 ACAGAGTTGA CGTAAGACCA GACAAGGACA TAGTCCCAGA AGACGTTCTGA GACCTTCCAT
 25 26 27

130 140 150 160 170 180
 TCTCTCCGGA ACTGGGTCCG ACTCTGGACA CTCTGCAGCT AGATGTAGCT GACTTTGCTA
 AGAGAGGCCT TGACCCAGGC TGAGACCTGT GAGACGTCGA TCTACATCGA CTGAACACGAT
 28 29

190 200 210
 CTAATAATTG GCAACAGATG GAAGAGCTCA AAG
 GATGATAAAC CGTGTCTAC CTCTCTCGAGT TTCTTTAA
 30 SstI EcoRI

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EChpG-CSFDNA SECTION III

10 31 20 30 40 50 60
 GATCCAAAG AGCTCGGTAT GGCACCAGCT CTGCAACCGA CTCAAGGTGC TATGCCGGCA
 GTTTC TCGAGCCATA CCGTGGTCTGA GACGTTGGCT GAGTTCCACG ATACGGCCGT

37

BamHI **SstI**

70 33 80 90 100 34 110 120
 TTTCGCTTCTG CATTCACGC TCGTGCAGGA GGTGTACTGG TTGCTTCTCA TCTGCAATCT
AAGCGAAGAC GTAAGGTCGC AGCAGTCCT CCACATGACC AACGAAGAGT AGACGTTAGA

39

35 130 140 150 160 170
 TTCCTGGAAG TATCTTACCG TGTTCTGCGT CATCTGGCTC AGCCGTAATA G
 AAGGACCTTC ATAGAATGGC ACAGACGCA GTAGACCGAG TCGGCATTAT CTAA
 41 42
 EcoRI

41

42

ECORI

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FIG. 7A

-1 +1
 Met Thr Pro Leu Gly Pro Ala Ser Ser Leu
 CTG TCT TCT Ser Ser Ala Pro Gly Leu Thr Met
 ATA TAA TAA AGG AGG CCA AAA TAG C

20
 CAG GGT AAA ATC CAG GGT GAC GGT GCT
 CCG CAA AGC TTT CTG CTG AAA TGT CTG GAA CAG
 pro Gln Ser Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala

40
 Leu Cys His Pro Glu Glu Leu Val Leu
 Lys Tyr Thr Ala Thr TAC TAC AAA CTG TGC CAT CCG GAA GAG CTG GTA CTG
 GCA CTG CAA GAA AAA CTG TGC GCT ACT ACT

60
 Leu Ser Cys Pro Ser Gln Ala Leu
 Gly His Ser Leu Gly Ile Pro Trp ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu
 CTG GGT CAT TCT CTT GGT ATC CCG TGG GCT CCG CTG TCT TCT TGT CCA TCT CAA GCT CTT

80
 Leu Ser Gly Leu Tyr Gln Gly Leu Leu
 Ala Gly Cys Leu Ser Gln leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu
 CAG CTG GCT GGT TGT CTG TCT CAA CTG CAT TCT TCT CTG TAT CAG GGT CTT CTG

100
 Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp
 CAA GCT CTG GAA GGT ATC TCT CCG GAA CTG GGT CCG ACT CTG GAC ACT CTG CAG CTA GAT

120
 Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu leu Gly Met Ala Pro Ala
 GTA GCT GAC TTT GCT ACT ACT ACT TTT TGG CAA CAG ATG GAG GAG CTC GGT ATG GCA CCA GCT

140
 Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly
 Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly
 CTG CAA CCG ACT CAA GGT GCT ATG CCG GCA TTC GCT TCT GCA TTC CAG CGT CGT GCA GGA

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FIG. 7B

[illegible]

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FIG. 8

1 ATCGATTGATTCTAGAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCCGGTACCAT
TAGCTAAACTAAGATCTTCCTCCTTATTGTATACCAATTGCGCAACCTTAAGCCATGGTA
1 Clal, 12 XbaI, 29 NdeI, 35 HincII, HpaI, 39 MluI, 47 EcoRI,
53 HgiCI KpnI, 57 NcoI SlyI,
61 GGAAGCTTACTCGAGGATCCGCGGATAAATAAGTAACGATCC
CCTTCGAATGAGCTCCTAGGCGCTATTTATTCATTTGCTAGG
63 HindIII, 70 AvaI XhoI, 75 BamHI Xho2, 79 Sac2,

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<u>Competitor</u>	<u>(U/ml)</u>	<u>WEHI-3B (D*)</u>		<u>ANLL (M4)</u>		<u>ANLL (M5B)</u>	
		<u>cpm</u>	<u>% Inhib.</u>	<u>cpm</u>	<u>% Inhib.</u>	<u>cpm</u>	<u>% Inhib.</u>
<u>Exp. 1</u>							
none	0	6,608	-	1,218	-	122	-
natural							
hpG-CSF:	10,000	685	90				
	2,000	1,692	74	34	97	-376	0
	200	2,031	69				
	10,000	0	100				
	2,000	1,185	82	202	83	0	0
	200	2,330	65				
<u>Exp. 2</u>							
none	0	2,910	0				
natural							
hpG-CSF:	2,000	628	78				
GM-CSF:	2,000	3,311	0				

FIG. 9